Amendments to the Claims

The current status of the claims is as follows:

1. (Original) A detection probe for use determining the presence of *Trichomonas vaginalis* in a test sample, said probe being up to 100 bases in length and comprising a target binding region which forms a hybrid stable for detection with a sequence contained within a first target sequence selected from the group consisting of SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3 and SEQ ID NO:4 under stringent hybridization conditions, wherein said probe does not form a hybrid stable for detection with nucleic acid derived from *Trichomonas tenax* under said conditions.

2. (Original) The probe of claim 1, wherein said target binding region comprises an at least 10 contiguous base region which is perfectly complementary to an at least 10 contiguous base region of said first target sequence.

3. (Original) The probe of claim 1, wherein said probe is up to 50 bases in length, and wherein said target binding region comprises an at least 15 contiguous base region which is perfectly complementary to an at least 15 contiguous base region of said first target sequence.

4. (Original) The probe of claim 1, wherein the base sequence of said target binding region is at least 80% complementary to the base sequence of said first target sequence.

5. (Original) The probe of claim 1, wherein the base sequence of said target binding region is at least 90% complementary to the base sequence of said first target sequence.

6. (Original) The probe of claim 1, wherein the base sequence of said target binding region is perfectly complementary to the base sequence of said first target sequence.

7. (Original) The probe of claim 1, wherein the base sequence of said probe consists of a base sequence which is at least about 80% complementary to the base sequence of said first target sequence.

8. (Original) The probe of claim 1, wherein the base sequence of said probe consists of a base sequence which is at least about 90% complementary to the base sequence of said first target sequence.

9. (Original) The probe of claim 1, wherein the base sequence of said probe consists of a base sequence which is perfectly complementary to the base sequence of said first target sequence.

10. (Original) The probe of claim 1, wherein the base sequence of said target binding region is perfectly complementary to all or a portion of said first target sequence, and wherein said probe does not comprise any other base sequences which stably hybridize to nucleic acid derived from *Trichomonas vaginalis* under said conditions.

11. (Original) The probe of claim 10, wherein said probe is a self-hybridizing probe under said conditions and in the absence of said first target sequence.

12. (Original) The probe of claim 11, wherein said probe comprises a pair of interacting labels.

13. (Original) The probe of claim 1, wherein said probe comprises a detectable label.

14. (Original) The probe of claim 1,wherein said target binding region includes at least one ribonucleotide modified to include a 2'-O-methyl substitution to the ribofuranosyl moiety.

15. (Original) The probe of claim 1, wherein a pseudo peptide backbone joins at least a portion of the bases of said target binding region.

16. (Original) The probe of claim 1, wherein said conditions include a temperature of about 60°C and a salt concentration of about 0.6 M to about 0.9 M.

17. (Original) A composition comprising said probe of claim 1 hybridized to nucleic acid derived from *Trichomonas vaginalis* under said conditions.

18. (Original) A probe mix comprising said probe of claim 1 and a helper probe.

19. (Original) The probe mix of claim 18, wherein said helper probe is up to 100 bases in length and comprises an at least 10 contiguous base region which is perfectly complementary to an at least 10 contiguous base region present in a second target sequence selected from the group consisting of SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25, SEQ ID NO:26, SEQ ID NO:27 and SEQ ID NO:28, wherein said helper probe stably hybridizes to said second target sequence under said conditions.

20. (Withdrawn) A method for determining the presence of *Trichomonas vaginalis* in a test sample, said method comprising the steps of:

a) contacting a test sample with said probe of claim 1 under said conditions; and

b) determining whether said hybrid is present in said test sample as indication of the presence of *Trichomonas vaginalis* in said test sample.

21. (Original) A detection probe for use determining the presence of *Trichomonas vaginalis* in a test sample, said probe being up to 100 bases in length and comprising a target binding region which forms a hybrid stable for detection with a sequence contained within a target sequence

selected from the group consisting of SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15 and SEQ ID NO:16 under stringent hybridization conditions, wherein said probe does not form a hybrid stable for detection with nucleic acid derived from *Trichomonas tenax* under said conditions.

22. (Original) The probe of claim 21, wherein said target binding region comprises an at least 10 contiguous base region which is perfectly complementary to an at least 10 contiguous base region of said target sequence.

23. (Original) The probe of claim 21, wherein said probe is up to 50 bases in length, and wherein said target binding region comprises an at least 15 contiguous base region which is perfectly complementary to an at least 15 contiguous base region of said target sequence.

24. (Original) The probe of claim 21, wherein the base sequence of said target binding region is at least 80% complementary to the base sequence of said first target sequence.

25. (Original) The probe of claim 21, wherein the base sequence of said target binding region is at least 90% complementary to the base sequence of said first target sequence.

26. (Original) The probe of claim 21, wherein the base sequence of said target binding region is perfectly complementary to the base sequence of said target sequence.

27. (Original) The probe of claim 21, wherein said target binding region comprises a base sequence which is perfectly complementary to a base sequence selected from the group consisting of SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19 and SEQ ID NO:20.

28. (Original) The probe of claim 21, wherein the base sequence of said probe consists of a base sequence which is at least about 80% complementary to the base sequence of said target sequence.

29. (Original) The probe of claim 21, wherein the base sequence of said probe consists of a base sequence which is at least about 90% complementary to the base sequence of said target sequence.

30. (Original) The probe of claim 21, wherein the base sequence of said probe consists of a base sequence which is perfectly complementary to the base sequence of said target sequence.

31. (Original) The probe of claim 21, wherein the base sequence of said target binding region is perfectly complementary to all or a portion of said target sequence, and wherein said probe does not comprise any other base sequences which stably hybridize to nucleic acid derived from *Trichomonas vaginalis* under said conditions.

32. (Original) The probe of claim 31, wherein said probe is a self-hybridizing probe under said conditions and in the absence of said target sequence.

33. (Original) The probe of claim 32, wherein said probe comprises a pair of interacting labels.

34. (Original) The probe of claim 21, wherein said probe comprises a detectable label.

35. (Original) The probe of claim 21,wherein said target binding region includes at least one ribonucleotide modified to include a 2'-O-methyl substitution to the ribofuranosyl moiety.

36. (Original) The probe of claim 21, wherein a pseudo peptide backbone joins at least a portion of the bases of said target binding region.

37. (Original) The probe of claim 21, wherein said conditions include a temperature of about 60°C and a salt concentration of about 0.6 M to about 0.9 M.

38. (Original) A composition comprising said probe of claim 21 hybridized to nucleic acid derived from *Trichomonas vaginalis* under said conditions.

39. (Withdrawn) A method for determining the presence of *Trichomonas vaginalis* in a test sample, said method comprising the steps of:

a) contacting a test sample with said probe of claim 21 under said conditions; and

b) determining whether said hybrid is present in said test sample as indication of the presence of *Trichomonas vaginalis* in said test sample.

Claims 40-76 (Canceled)

77. (New) A kit for use in determining the presence of *Trichomonas vaginalis* in a test sample, said kit comprising:

a detection probe up to 100 bases in length and comprising a first target binding region which forms a hybrid stable for detection with a sequence contained within a first target sequence selected from the group consisting of SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3 and SEQ ID NO:4 under stringent hybridization conditions, wherein said probe does not form a hybrid stable for detection with nucleic acid derived from *Trichomonas tenax* under said conditions; and

a capture probe up to 100 bases in length and comprising a second target binding region which stably hybridizes to nucleic acid derived from *Trichomonas vaginalis* under assay conditions, and wherein said capture probe has an at least 10 contiguous base region which is perfectly

complementary to an at least 10 contiguous base region present in a second target sequence selected from the group consisting of SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:31 and SEQ ID NO:32.

78. (New) The kit of claim 77 further comprising a helper probe up to 100 bases in length and comprising an at least 10 contiguous base region which is perfectly complementary to an at least 10 contiguous base region present in a third target sequence selected from the group consisting of SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25, SEQ ID NO:26, SEQ ID NO:27 and SEQ ID NO:28, wherein said helper probe stably hybridizes to said third target sequence under said stringent hybridization conditions.

79. (New) A kit for use in determining the presence of *Trichomonas vaginalis* in a test sample, said kit comprising:

a detection probe for use determining the presence of *Trichomonas vaginalis* in a test sample, said probe being up to 100 bases in length and comprising a first target binding region which forms a hybrid stable for detection with a sequence contained within a first target sequence selected from the group consisting of SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15 and SEQ ID NO:16 under stringent hybridization conditions, wherein said probe does not form a hybrid stable for detection with nucleic acid derived from *Trichomonas tenax* under said conditions; and

a capture probe up to 100 bases in length and comprising a second target binding region which stably hybridizes to nucleic acid derived from *Trichomonas vaginalis* under assay conditions, and wherein said capture probe has an at least 10 contiguous base region which is perfectly complementary to an at least 10 contiguous base region present in a second target sequence selected from the group consisting of SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:31 and SEQ ID NO:32.

80. (New) The kit of claim 79, wherein said first target binding region comprises a base sequence which is perfectly complementary to a base sequence selected from the group consisting of SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19 and SEQ ID NO:20.